

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
 Yue, Henry  
 Lal, Preeti  
 Shah, Purvi  
 Corley, Neil C.

(ii) TITLE OF THE INVENTION: PROTEINS ASSOCIATED WITH CELL  
 PROLIFERATION

(iii) NUMBER OF SEQUENCES: 9

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 (B) STREET: 3174 Porter Dr.  
 (C) CITY: Palo Alto  
 (D) STATE: CA  
 (E) COUNTRY: USA  
 (F) ZIP: 94304

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
 (B) COMPUTER: IBM Compatible  
 (C) OPERATING SYSTEM: DOS  
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
 (B) FILING DATE: Filed Herewith

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
 (B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
 (B) REGISTRATION NUMBER: 36,749  
 (C) REFERENCE/DOCKET NUMBER: PF-0421 US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
 (B) TELEFAX: 650-845-4166

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: SYNORAB01  
 (B) CLONE: 358673

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Gln	Ile	Pro	Glu	Phe	Glu	Pro	Ser	Glu	Gln	Glu	Asp	Ser	Ser
1				5				10						15	
Ser	Ala	Glu	Arg	Gly	Leu	Gly	Pro	Ser	Pro	Ala	Gly	Asp	Gly	Pro	Ser
			20					25					30		

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala  
 35 40 45  
 Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala  
 50 55 60  
 Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr  
 65 70 75 80  
 Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg  
 85 90 95  
 Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg  
 100 105 110  
 Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly  
 115 120 125  
 Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser  
 130 135 140  
 Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly  
 145 150 155 160  
 Arg Gly Ser Ser Ala Pro Ser Gln  
 165

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: 358673  
 (B) CLONE: SYNORAB01

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGACCGTCCG	CGGGAGACTG	AGGTCCTGAG	CCGACAGCCT	CAGCTCCCTG	CCAGGCCAGA	60
CCCGGCAGAC	AGATGAGGGC	CCAGGAGGCC	TGGCGGGCCT	GGGGGCGCTA	CGGTGGGAGA	120
GGAAGCCAGG	GGTACCTGCC	TCTGCCTTCC	AGGGCCACCG	TTGGCCCCAG	CTGTGCCTTG	180
ACTACGTAAC	ATCTTGTCCT	CACAGCCCAG	AGCATGTTCC	AGATCCCAGA	GTTTGAGCCG	240
AGTGAGCAGG	AAGACTCCAG	CTCTGCAGAG	AGGGGCTTGG	GCCCCAGCCC	CGCAGGGGAC	300
GGGCCCTCAG	GCTCCGGCAA	GCATCATCGC	CAGGCCCCAG	GCCTCCTGTG	GGACGCCAGT	360
CACCAGCAGG	AGCAGCCAAC	CAGCAGCAGC	CATCATGGAG	GCGCTGGGGC	TGTGGAGATC	420
CGGAGTCGCC	ACAGCTCCTA	CCCCGCGGGG	ACGGAGGACG	ACGAAGGGAT	GGGGGAGGAG	480
CCCAGCCCCCT	TCGGGGGCGG	CTCGCGCTCG	GCGCCCCCCA	ACCTCTGGGC	AGCACAGCGC	540
TATGGCCGCG	AGCTCCGGAG	GATGAGTGAC	GAGTTTGTGG	ACTCCTTTAA	GAAGGGACTT	600
CCTCGCCCGA	AGAGCGCGGG	CACAGCAACG	CAGATGCGGC	AAAGCTCCAG	CTGGACGCGA	660
GTCTTCCAGT	CCTGGTGGGA	TCGGAACCTG	GGCAGGGGAA	GCTCCGCCCC	CTCCCAGTGA	720
CCTTCGCTCC	ACATCCCGAA	ACTCCACCCG	TTCCCCTGTC	CCTGGGCAGC	CATCTTGAAT	780
ATGGGCGGAA	GTACTTCCCT	CAGGCCTATG	CAAAAAGAGG	ATCCGTGCTG	TCTCCTTTGG	840
AGGGAGGGCT	GACCCAGATT	CCCTTCCGGT	GCGTGTGAAG	CCACGGAAGG	CTTGGTCCCA	900
TCGGAAGTTT	TGGGTTTTC	GCCCACAGCC	GCCGGAAGTG	GCTCCGTGGC	CCCGCCCTCA	960
GGCTCCGGGC	TTTCCCCCAG	GCGCCTGCGC	TAAGTCGCGA	GCCAGGTTTA	ACCGTTGCGT	1020
CACCGGGACC	CGAGCCCCCG	CGATGCCCTG	GGGGCCGTGC	TCACTACCAA	ATGTTAATAA	1080
AGCCCGCGTC	TGTGCAAAAA	AAAAA				1105

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02  
 (B) CLONE: 1352286

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala  
 1 5 10 15  
 Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His  
 20 25 30  
 Gly Arg Ala Gly Gly Gly Arg Arg Gly Ser Asn Pro Val Lys Arg Tyr  
 35 40 45  
 Ala Pro Gly Leu Pro Cys Asp Val Tyr Thr Tyr Leu His Glu Lys Tyr  
 50 55 60  
 Leu Asp Cys Gln Glu Arg Lys Leu Val Tyr Val Leu Pro Gly Trp Pro  
 65 70 75 80  
 Gln Asp Leu Leu His Met Leu Leu Ala Arg Asn Lys Ile Arg Thr Leu  
 85 90 95  
 Lys Asn Asn Met Phe Ser Lys Phe Lys Lys Leu Lys Ser Leu Asp Leu  
 100 105 110  
 Gln Gln Asn Glu Ile Ser Lys Ile Glu Ser Glu Ala Phe Phe Gly Leu  
 115 120 125  
 Asn Lys Leu Thr Thr Leu Leu Gln His Asn Gln Ile Lys Val Leu  
 130 135 140  
 Thr Glu Glu Val Phe Ile Tyr Thr Pro Leu Leu Ser Tyr Leu Arg Leu  
 145 150 155 160  
 Tyr Asp Asn Pro Trp His Cys Thr Cys Glu Ile Glu Thr Leu Ile Ser  
 165 170 175  
 Met Leu Gln Ile Pro Arg Asn Arg Asn Leu Gly Asn Tyr Ala Lys Cys  
 180 185 190  
 Glu Ser Pro Gln Glu Gln Lys Asn Lys Lys Leu Arg Gln Ile Lys Ser  
 195 200 205  
 Glu Gln Leu Cys Asn Glu Glu Lys Glu Gln Leu Asp Pro Lys Pro Gln  
 210 215 220  
 Val Ser Gly Arg Pro Pro Val Ile Lys Pro Glu Val Asp Ser Thr Phe  
 225 230 235 240  
 Cys His Asn Tyr Val Phe Pro Ile Gln Thr Leu Asp Cys Lys Arg Lys  
 245 250 255  
 Glu Leu Lys Lys Val Pro Asn Asn Ile Pro Pro Asp Ile Val Lys Leu  
 260 265 270  
 Asp Leu Ser Tyr Asn Lys Ile Asn Gln Leu Arg Pro Lys Glu Phe Glu  
 275 280 285  
 Asp Val His Glu Leu Lys Lys Leu Asn Leu Ser Ser Asn Gly Ile Glu  
 290 295 300  
 Phe Ile Asp Pro Ala Ala Phe Leu Gly Leu Thr His Leu Glu Glu Leu  
 305 310 315 320  
 Asp Leu Ser Asn Asn Ser Leu Gln Asn Phe Asp Tyr Gly Val Leu Glu  
 325 330 335  
 Asp Leu Tyr Phe Leu Lys Leu Leu Trp Leu Arg Asp Asn Pro Trp Arg  
 340 345 350  
 Cys Asp Tyr Asn Ile His Tyr Leu Tyr Tyr Trp Leu Lys His His Tyr  
 355 360 365  
 Asn Val His Phe Asn Gly Leu Glu Cys Lys Thr Pro Glu Glu Tyr Lys  
 370 375 380  
 Gly Trp Ser Val Gly Lys Tyr Ile Arg Ser Tyr Tyr Glu Glu Cys Pro  
 385 390 395 400  
 Lys Asp Lys Leu Pro Ala Tyr Pro Glu Ser Phe Asp Gln Asp Thr Glu  
 405 410 415  
 Asp Asp Glu Trp Glu Lys Lys His Arg Asp His Thr Ala Lys Lys Gln  
 420 425 430  
 Ser Val Ile Ile Thr Ile Val Gly  
 435 440

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: LATRTUT02

(B) CLONE: 1352286

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATGCAGCC CATTCTCTGG AGAACTTCCT CACACACCGC AGCAAAGAGA AGACTGAAAG 60  
 ACAAACCTGG GTGCAGCCAG AGAGGTCCAG ATAGATGAGC TTGTGGCATC CATTCCCCAA 120  
 GTTCAGCCTA GGGACTCCAC GTACCCACAG TGGGTCTCAT TGTTCAGAA CTGCATTAGT 180  
 TAAGATTACC CAGACTTGGA TTTCAAAGGA ATACTTTTCAT TGTTCGCTCT GTAACACGAA 240  
 GTAATTGGGG CCAGCTGGAT GTCAGGATGC GTGTGGTTAC CATTGTAATC TTGCTCTGCT 300  
 TTTGCAAAGC GGCTGAGCTG CGCAAAGCAA GCCCAGGCAG TGTGAGAAGC CGAGTGAATC 360  
 ATGGCCGGGC GGGTGGAGGC CGGAGAGGCT CCAACCCGGT CAAACGCTAC GCACCAGGCC 420  
 TCCCGTGTGA CGTGACACA TATCTCCATG AGAAATACCT AGATTGTCAA GAAAGAAAAT 480  
 TAGTTTATGT GCTGCCTGGT TGGCCTCAGG ATTTGCTGCA CATGCTGCTA GCAAGAAACA 540  
 AGATCCGCAC ATTGAAGAAC AACATGTTTT CCAAGTTTAA AAAGCTGAAA AGCCTGGATC 600  
 TGCAGCAGAA TGAGATCTCT AAAATTGAGA GTGAGGCGTT CTTTGGTTTA AACAAACTCA 660  
 CCACCTCTTT ACTGCAGCAC AACCAGATCA AAGTCTTGAC GGAGGAAGTG TTCATTTACA 720  
 CACCTCTCTT GAGCTACCTG CGTCTTTATG ACAACCCCTG GCACTGTACT TGTGAGATAG 780  
 AAACGCTTAT TTCAATGTTG CAGATTCCCA GGAACCGGAA TTTGGGGAAC TACGCCAAGT 840  
 GTGAAAGTCC ACAAGAACA AAAAATAAAA AACTGCGGCA GATAAAATCT GAACAGTTGT 900  
 GTAATGAAGA AAAGGAACAA TTGGACCCGA AACCCCAAGT GTCAGGGAGA CCCCCAGTCA 960  
 TCAAGCCTGA GGTGGACTCA ACTTTTTGCG ACAATTATGT GTTTCCCATA CAAACACTGG 1020  
 ACTGCAAAAAG GAAAGAGTTG AAAAAAGTGC CAAACAACAT CCCTCCAGAT ATTGTTAAAC 1080  
 TTGACTTGTC ATACAATAAA ATCAACCAAC TTCGACCCAA GGAATTTGAA GATGTTTCATG 1140  
 AGCTGAAGAA ATTAAACCTC AGCAGCAATG GCATTGAATT CATCGATCCT GCCGCTTTTT 1200  
 TAGGGCTCAC ACATTTAGAA GAATTAGATT TATCAAACAA CAGTCTGCAA AACTTTGACT 1260  
 ATGGCGTATT AGAAGACTTG TATTTTTTGA AACTCTTGTC GCTCAGAGAT AACCTTGGA 1320  
 GATGTGACTA CAACATTCAC TACCTCTACT ACTGGTTAAA GCACCACTAC AATGTCCATT 1380  
 TTAATGGCCT GGAATGCAAA ACGCCTGAAG AATACAAAGG ATGGTCTGTG GGAAAATATA 1440  
 TTAGAAGTTA CTATGAAGAA TGCCCCAAAG ACAAGTTACC AGCATATCCT GAGTCATTTG 1500  
 ACCAAGACAC AGAAGATGAT GAATGGGAAA AAAAACATAG AGATCACACC GCAAAGAAGC 1560  
 AAAGCGTAAT AATTACTATA GTAGGATAAG GTAGAAATTG TTCTGATTGT AATTAGTTTT 1620  
 GTATTTTCTA TACTGGTGTT AGAAAACATA TGTTTACATT TGATTAACCTG TGTTGCCTAT 1680  
 TTATGCAGGG TAATCCAGCT AAAGGAAGCT TTCTTTAATT ATAAGTATTA TTGTGACTAT 1740  
 TATAGTAATC AAGAGAATGC TATCATCCTG CTTGCCTGTC CATTTGTGGA ACAGCATCTG 1800  
 GTGATATGCA ATTCCACACT GGTAACCTGC AGCAGTTGGG TCCTAATGAT GGCATTAGAC 1860  
 TTTTATAATG TCCTGTATA ATGTTTTTAC TGCTTTTAGA AAATAAAGAA AAAAACTTG 1920  
 GTTCATGTTT ACATGCCTTT CGATAGCTGT TTGTGCATAC TTAAAGATGA TCAAAATGAT 1980  
 TTTATACAAA TGCTGTTATA ATAAAATGTC ATTCCCTACC CCTCTACTTT TTTTCAGTAA 2040  
 GTCATCTTAT ACATTAAATA AATTTCCATT TCTGAAAAAA AA 2082

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT01  
 (B) CLONE: 815087

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Val Glu Asn Glu Gln Ile Leu Asn Val Asn Pro Ala Asp Pro  
 1 5 10 15  
 Asp Asn Leu Ser Asp Ser Leu Phe Ser Gly Asp Glu Glu Asn Ala Gly  
 20 25 30  
 Thr Glu Glu Val Lys Asn Glu Ile Asn Gly Asn Trp Ile Ser Ala Ser  
 35 40 45  
 Ser Ile Asn Glu Ala Arg Ile Asn Ala Lys Ala Lys Arg Arg Leu Arg  
 50 55 60  
 Lys Asn Ser Ser Arg Asp Ser Gly Arg Gly Asp Ser Val Ser Asp Ser  
 65 70 75 80  
 Gly Ser Asp Ala Leu Arg Ser Gly Leu Thr Val Pro Thr Ser Pro Lys

85 90 95  
 Gly Arg Leu Leu Asp Arg Arg Ser Arg Ser Gly Lys Gly Arg Gly Leu  
 100 105 110  
 Pro Lys Lys Gly Gly Ala Gly Gly Lys Gly Val Trp Gly Thr Pro Gly  
 115 120 125  
 Gln Val Tyr Asp Val Glu Glu Val Asp Val Lys Asp Pro Asn Tyr Asp  
 130 135 140  
 Asp Asp Gln Glu Asn Cys Val Tyr Glu Thr Val Val Leu Pro Leu Asp  
 145 150 155 160  
 Glu Arg Ala Phe Glu Lys Thr Leu Thr Pro Ile Ile Gln Glu Tyr Phe  
 165 170 175  
 Glu His Gly Asp Thr Asn Glu Val Ala Glu Met Leu Arg Asp Leu Asn  
 180 185 190  
 Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu Ala Val Ser Leu Ala  
 195 200 205  
 Leu Glu Gly Lys Ala Ser His Arg Glu Met Thr Ser Lys Leu Leu Ser  
 210 215 220  
 Asp Leu Cys Gly Thr Val Met Ser Thr Thr Asp Val Glu Lys Ser Phe  
 225 230 235 240  
 Asp Lys Leu Leu Lys Asp Leu Pro Glu Leu Ala Leu Asp Thr Pro Arg  
 245 250 255  
 Ala Pro Gln Leu Val Gly Gln Phe Ile Ala Arg Ala Val Gly Asp Gly  
 260 265 270  
 Ile Leu Cys Asn Thr Tyr Ile Asp Ser Tyr Lys Gly Thr Val Asp Cys  
 275 280 285  
 Val Gln Ala Arg Ala Ala Leu Asp Lys Ala Thr Val Leu Leu Ser Met  
 290 295 300  
 Ser Lys Gly Gly Lys Arg Lys Asp Ser Val Trp Gly Ser Gly Gly Gly  
 305 310 315 320  
 Gln Gln Ser Val Asn His Leu Val Lys Glu Ile Asp Met Leu Leu Lys  
 325 330 335  
 Glu Tyr Leu Leu Ser Gly Asp Ile Ser Glu Ala Glu His Cys Leu Lys  
 340 345 350  
 Glu Leu Glu Val Pro His Phe His His Glu Leu Val Tyr Glu Ala Ile  
 355 360 365  
 Ile Met Val Leu Glu Ser Thr Gly Glu Ser Thr Phe Lys Met Ile Leu  
 370 375 380  
 Asp Leu Leu Lys Ser Leu Trp Lys Ser Ser Thr Ile Thr Val Asp Gln  
 385 390 395 400  
 Met Lys Arg Gly Tyr Glu Arg Ile Tyr Asn Glu Ile Pro Asp Ile Asn  
 405 410 415  
 Leu Asp Val Pro His Ser Tyr Ser Val Leu Glu Arg Phe Val Glu Glu  
 420 425 430  
 Cys Phe Gln Ala Gly Ile Ile Ser Lys Gln Leu Arg Asp Leu Cys Pro  
 435 440 445  
 Ser Arg Gly Arg Lys Arg Phe Val Ser Glu Gly Asp Gly Gly Arg Leu  
 450 455 460  
 Lys Pro Glu Ser Tyr  
 465

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT01
- (B) CLONE: 815087

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACAGCTCGAG CTCGAGCCGC AAAACTGTCT GCAGACGTCA ATTCGCCCC CCTCCCCCTT 60  
 GTGAGAACTC GCTACGTAGC CAGCAACTGT GTAGTGTCTA CAAATGATGA AAACGATCAG 120

AAATGCGATT AGGTGTCGGG GAAAAAAGGG TTTCCCCTGT TTTTAACTTG TATTTTTACT 180  
 TTAATTGTGA CAATCTTGAT ATTCTTAACG TGACTTTTTT GGGAAACCAC CAAGTGCTTT 240  
 TTAAGCAAGG AGTTACTGAT TCTGAAGGAA GATTTCCATT AGGTAATTTG TTTAATCAGT 300  
 GCAAGCGAAA TTAAGGGAAA ATGGATGTAG AAAATGAGCA GATACTGAAT GTAAACCCTG 360  
 CAGATCCTGA TAACTTAAGT GACTCTCTCT TTTCCGGTGA TGAAGAAAAT GCTGGGACTG 420  
 AGGAAGTAAA GAATGAAATA AATGGAAATT GGATTTTCAGC ATCCTCCATT AACGAAGCTA 480  
 GAATTAATGC CAAGGCAAAA AGGCGACTAA GGAAAACTC ATCCCGGGAC TCTGGCAGAG 540  
 GCGATTCGGT CAGCGACAGT GGGAGTGACG CCCTTAGAAG TGGATTAAC TGTGCCAACCA 600  
 GTCCAAAGGG AAGGTTGCTG GATAGGCGAT CCAGATCTGG GAAAGGAAGG GGAATACCA 660  
 AGAAAGGTGG TGCAGGAGGC AAAGGTGTCT GGGGTACACC TGGACAGGTG TATGATGTGG 720  
 AGGAGGTGGA TGTGAAAGAT CCTAACTATG ATGATGACCA GGAGAACTGT GTTTATGAAA 780  
 CTGTAGTTTT GCCTTTGGAT GAAAGGGCAT TTGAGAAGAC TTTAACACCA ATCATACAGG 840  
 AATATTTTGA GCATGGAGAT ACTAATGAAG TTGCGGAAAT GTTAAGAGAT TTAATCTTG 900  
 GTGAAATGAA AAGTGGAGTA CCAGTGTGG CAGTATCCTT AGCATTGAG GGAAGGCTA 960  
 GTCATAGAGA GATGACATCT AAGCTTCTTT CTGACCTTTG TGGGACAGTA ATGAGCACAA 1020  
 CTGATGTGGA AAAATCATTT GATAAATTGT TGAAAGATCT ACCTGAATTA GCACTGGATA 1080  
 CTCCTAGAGC ACCACAGTTG GTGGGCCAGT TTATTGCTAG AGCTGTTGGA GATGGAATTT 1140  
 TATGTAATAC CTATATTGAT AGTTACAAAG GAACGTGAGA TTGTGTGCAG GCTAGAGCTG 1200  
 CTCTGGATAA GGCTACCGTG CTTCTGAGTA TGTCTAAAGG TGGAAAGCGT AAAGATAGTG 1260  
 TGTGGGGCTC TGGAGGTGGG CAGCAATCTG TCAATCACCT TGTTAAAGAG ATTGATATGC 1320  
 TGCTGAAAGA ATATTTACTC TCTGGAGACA TATCTGAAGC TGAACATTGC CTTAAGGAAC 1380  
 TGGAAGTACC TCATTTTCAC CATGAGCTTG TATATGAAGC TATTATAATG GTTTTAGAGT 1440  
 CAACTGGAGA AAGTACATTT AAGATGATTT TGGATTTATT AAAGTCCCTT TGGAAAGTCTT 1500  
 CTACCATTAC TGTAGACCAA ATGAAAAGAG GTTATGAGAG AATTTACAAT GAAATTCCGG 1560  
 ACATTAATCT GGATGTCCCA CATTCATACT CTGTGCTGGA GCGGTTTGTA GAAGAATGTT 1620  
 TTCAGGCTGG AATAATTTCC AAACAACCTCA GAGATCTTTG TCCTTCAAGG GGCAGAAAGC 1680  
 GTTTTGTAAG CGAAGGAGAT GGAGGTCGTC TTAAACCAGA GAGCTACTGA ATATAAGAAC 1740  
 TCTTGCAGTC TTAGATGTTA TAAAAATATA TATCTGAATT GTAAGAGTTG TTAGCACAAG 1800  
 TTTTTTTTTT TTTTTTTTTT TAAGCACTTG TTTTGGGTAC AAGGCATTC TGACATTTTA 1860  
 TAAACCTACA TTTAAGGGGA ATTTTAAAG GAAATGTTTT TTCTTTTTTT TTTGTTTTTC 1920  
 GAGGGGGCAA GGAGGGACAG AAAAGTAACC TCTTCTTAAG TGGAATATTC TAATAAGCTA 1980  
 CCTTTTGTA GTGCCATGTT TATATCTAA TCATTCCAAG TTTTGCATTG ATGTCTGACT 2040  
 GCCACTCCTT TCTTTCAAG ACAGTGTFTT TTGTAGTAAA ATCACTGGTT TATACAAAGC 2100  
 TTTATTTAGG GGGTAAAGTT AAGCTGCTAA AACCCCATGT TGGCTGCTGC TGTTGAGATA 2160  
 CTGTGCTTTG GGAGTAAAAA AAGAAAGTTA TTTCTTTGTC TTAAAGAATT TTTAAAAAAT 2220  
 TAGTCATGAG ACTTATTCAT CTTTCCAGGG AACATACTGA TTGGTCTTAA AAGACTAGAC 2280  
 AGTTAAGTAA AAGGTGGCTG GAACATCTAT TTTTCTACAA AACTGGAAAA ATGAACCTGG 2340  
 TTCTAGAAGA ATGTACACCA AAATAAAACA TGTGAAGCAG TATTGAAAAA AAAAA 2395

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1683637

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser  
 1 5 10 15  
 Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser  
 20 25 30  
 Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala  
 35 40 45  
 Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Arg  
 50 55 60  
 Trp Gly Cys Gly Asp Pro Glu Ser Pro Gln Leu Leu Pro Arg Gly Asp  
 65 70 75 80  
 Gly Gly Arg Arg Arg Asp Gly Gly Gly Ala Gln Pro Phe Arg Gly Arg  
 85 90 95  
 Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg

```

      100      105      110
Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
      115      120      125
Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
      130      135      140
Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
145      150      155      160
Arg Gly Ser Ser Ala Pro Ser Gln
      165

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1236329

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala
 1      5      10      15
Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His
      20      25      30
Gly Arg Ala Gly Gly Gly Arg Arg Gly Ser Asn Pro Val Lys Arg Tyr
      35      40      45

Ala Pro Gly Leu Pro Cys Asp Val Tyr Thr Tyr Leu His Glu Lys Tyr
 50      55      60
Leu Asp Cys Gln Glu Arg Lys Leu Val Tyr Val Leu Pro Gly Trp Pro
 65      70      75      80
Gln Asp Leu Leu His Met Leu Leu Ala Arg Asn Lys Ile Arg Thr Leu
      85      90      95
Lys Asn Asn Met Phe Ser Lys Phe Lys Lys Leu Lys Ser Leu Asp Leu
      100      105      110
Gln Gln Asn Glu Ile Ser Lys Ile Glu Ser Glu Ala Phe Phe Gly Leu
      115      120      125
Asn Lys Leu Thr Thr Leu Leu Leu Gln His Asn Gln Ile Lys Val Leu
      130      135      140
Thr Glu Glu Val Phe Ile Tyr Thr Pro Leu Leu Ser Tyr Leu Arg Leu
145      150      155      160
Tyr Asp Asn Pro Trp His Cys Thr Cys Glu Ile Glu Thr Leu Ile Ser
      165      170      175
Met Leu Gln Ile Pro Arg Asn Arg Asn Leu Ala Asn Tyr Ala Lys Cys
      180      185      190
Glu Ser Pro Gln Glu Gln Lys Asn Lys Lys Leu Arg Gln Ile Lys Ser
      195      200      205
Glu Gln Leu Cys Asn Glu Glu Glu Lys Glu Gln Leu Asp Pro Lys Pro
      210      215      220
Gln Val Ser Gly Arg Pro Pro Val Ile Lys Pro Glu Val Asp Ser Thr
225      230      235      240
Phe Cys His Asn Tyr Val Phe Pro Ile Gln Thr Leu Asp Cys Lys Arg
      245      250      255
Lys Glu Leu Lys Lys Val Pro Asn Asn Ile Pro Pro Asp Ile Val Lys
      260      265      270
Leu Asp Leu Ser Tyr Asn Lys Ile Asn Gln Leu Arg Pro Lys Glu Phe
      275      280      285
Glu Asp Val His Glu Leu Lys Lys Leu Asn Leu Ser Ser Asn Gly Ile
      290      295      300
Glu Phe Ile Asp Pro Gly Ser Leu Arg
305      310

```

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1384078

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Asp	Ile	Glu	Asn	Glu	Gln	Thr	Leu	Asn	Val	Asn	Pro	Thr	Asp	Pro
1				5					10					15	
Asp	Asn	Leu	Ser	Asp	Ser	Leu	Phe	Ser	Gly	Asp	Glu	Glu	Asn	Ala	Gly
			20					25					30		
Thr	Glu	Glu	Ile	Lys	Asn	Glu	Ile	Asn	Gly	Asn	Trp	Ile	Ser	Ala	Ser
			35				40					45			
Thr	Ile	Asn	Glu	Ala	Arg	Ile	Asn	Ala	Lys	Ala	Lys	Arg	Arg	Leu	Arg
	50					55					60				
Lys	Asn	Ser	Ser	Arg	Asp	Ser	Gly	Arg	Gly	Asp	Ser	Val	Ser	Asp	Asn
65					70					75					80
Gly	Ser	Glu	Ala	Val	Arg	Ser	Gly	Val	Ala	Val	Pro	Thr	Ser	Pro	Lys
				85				90						95	
Gly	Arg	Leu	Leu	Asp	Arg	Arg	Ser	Arg	Ser	Gly	Lys	Gly	Arg	Gly	Leu
			100					105					110		
Pro	Lys	Lys	Gly	Gly	Ala	Gly	Gly	Lys	Gly	Val	Trp	Gly	Thr	Pro	Gly
			115				120					125			
Gln	Val	Tyr	Asp	Val	Glu	Glu	Val	Asp	Val	Lys	Asp	Pro	Asn	Tyr	Asp
						135					140				
Asp	Asp	Gln	Glu	Asn	Cys	Val	Tyr	Glu	Thr	Val	Val	Leu	Pro	Leu	Asp
145					150					155					160
Glu	Thr	Ala	Phe	Glu	Lys	Thr	Leu	Thr	Pro	Ile	Ile	Gln	Glu	Tyr	Phe
				165				170						175	
Glu	His	Gly	Asp	Thr	Asn	Glu	Val	Ala	Glu	Met	Leu	Arg	Asp	Leu	Asn
			180					185					190		
Leu	Gly	Glu	Met	Lys	Ser	Gly	Val	Pro	Val	Leu	Ala	Val	Ser	Leu	Ala
			195				200					205			
Leu	Glu	Gly	Lys	Ala	Ser	His	Arg	Glu	Met	Thr	Ser	Lys	Leu	Leu	Ser
						215					220				
Asp	Leu	Cys	Gly	Thr	Val	Met	Ser	Thr	Asn	Asp	Val	Glu	Lys	Ser	Phe
225					230					235					240
Asp	Lys	Leu	Leu	Lys	Asp	Leu	Pro	Glu	Leu	Ala	Leu	Asp	Thr	Pro	Arg
				245				250						255	
Ala	Pro	Gln	Leu	Val	Gly	Gln	Phe	Ile	Ala	Arg	Ala	Val	Gly	Asp	Gly
				260				265					270		
Ile	Leu	Cys	Asn	Thr	Tyr	Ile	Asp	Ser	Tyr	Lys	Gly	Thr	Val	Asp	Cys
			275				280					285			
Val	Gln	Ala	Arg	Ala	Ala	Leu	Asp	Lys	Ala	Thr	Val	Leu	Leu	Ser	Met
						295					300				
Ser	Lys	Gly	Gly	Lys	Arg	Lys	Asp	Ser	Val	Trp	Gly	Ser	Gly	Gly	Gly
305					310					315					320
Gln	Gln	Pro	Val	Asn	His	Leu	Val	Lys	Glu	Ile	Asp	Met	Leu	Leu	Lys
				325					330					335	
Glu	Tyr	Leu	Leu	Ser	Gly	Asp	Ile	Ser	Glu	Ala	Glu	His	Cys	Leu	Lys
				340				345					350		
Glu	Leu	Glu	Val	Pro	His	Phe	His	His	Glu	Leu	Val	Tyr	Glu	Ala	Ile
				355			360					365			
Val	Met	Val	Leu	Glu	Ser	Thr	Gly	Glu	Ser	Ala	Phe	Lys	Met	Ile	Leu
						375					380				
Asp	Leu	Leu	Lys	Ser	Leu	Trp	Lys	Ser	Ser	Thr	Ile	Thr	Ile	Asp	Gln
385					390					395					400
Met	Lys	Arg	Gly	Tyr	Glu	Arg	Ile	Tyr	Asn	Glu	Ile	Pro	Asp	Ile	Asn
				405					410					415	



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Leu Asp Val Pro His Ser Tyr Ser Val Leu Glu Arg Phe Val Glu Glu  
420 425 430  
Cys Phe Gln Ala Gly Ile Ile Ser Lys Gln Leu Arg Asp Leu Cys Pro  
435 440 445  
Ser Arg Gly Arg Lys Arg Phe Val Ser Glu Gly Asp Gly Gly Arg Leu  
450 455 460  
Lys Pro Glu Ser Tyr  
465

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